


L Number	Hits	Search Text	DB	Time stamp
1	133	coxsackievirus near3 adenovirus near3 receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:24
2	626	car and adenovirus	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
3	4	cxadr	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
4	0	cvb3 adj binding adj protein	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
5	731	(coxsackievirus near3 adenovirus near3 receptor) or (car and adenovirus) or cxadr or (cvb3 adj binding adj protein)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:25
6	483	((coxsackievirus near3 adenovirus near3 receptor) or (car and adenovirus) or cxadr or (cvb3 adj binding adj protein)) and (pig or porcine)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:26
7	77107	pig or porcine	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:27
8	0	(coxsackievirus near3 adenovirus near3 receptor) near10 (pig or porcine)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:27
9	29	PCAR	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:28
10	0	PCAR AND ADENOVIRUS	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:29
11	456	((((coxsackievirus near3 adenovirus near3 receptor) or (car and adenovirus) or cxadr or (cvb3 adj binding adj protein)) and (pig or porcine)) AND ("NUCLEIC ACID" OR DNA)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:32
12	0	(coxsackievirus near3 adenovirus near3 receptor) NEAR5 (pig or porcine)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:32
13	154	(pig or porcine) NEAR5 CAR	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:33
14	1	((pig or porcine) NEAR5 CAR) AND COXSACKIEVIRUS	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:34
15	0	(pig or porcine) NEAR5 CVB3	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:35
16	0	(pig or porcine) NEAR5 CXADR	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/07 14:35

(FILE 'HOME' ENTERED AT 14:04:56 ON 07 AUG 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, CANCERLIT' ENTERED AT 14:07:29 ON
07 AUG 2003

L1	834 S COXSACKIEVIRUS (3A) ADENOVIRUS
L2	628 S L1 (3A) RECEPTOR
L3	5 S CXADR
L4	1178 S CAR AND ADENOVIRUS
L5	572 S L4 AND COXSACKIEVIRUS
L6	1115 S CVB3
L7	5 S CVB3 BINDING PROTEIN
L8	2374 S L2 OR L4 OR L3 OR L6
L9	27 S L8 AND (PIG OR PORCINE)
L10	10 DUP REM L9 (17 DUPLICATES REMOVED)

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Entry information

Entry name	CXAR_HUMAN
Primary accession number	P78310
Secondary accession number	O00694
Entered in Swiss-Prot in	Release 39, May 2000
Sequence was last modified in	Release 39, May 2000
Annotations were last modified in	Release 42, September 2003
Name and origin of the protein	
Protein name	Coxsackievirus and adenovirus receptor [Precursor]
Synonyms	Coxsackievirus B-adenovirus receptor hCAR CVB3 binding protein
Gene name	CXADR or CAR
From	<u>Homo sapiens (Human)</u> [TaxID: 9606]
Taxonomy	<u>Eukaryota</u> ; <u>Metazoa</u> ; <u>Chordata</u> ; <u>Craniata</u> ; <u>Vertebrata</u> ; <u>Euteleostomi</u> ; <u>Mammalia</u> ; <u>Eutheria</u> ; <u>Primates</u> ; <u>Catarrhini</u> ; <u>Hominidae</u> ; <u>Homo</u> .

References

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- [2] SEQUENCE FROM NUCLEIC ACID.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Comments

- **FUNCTION:** SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
- **SUBCELLULAR LOCATION:** Type I membrane protein.
- **SIMILARITY:** Contains 2 immunoglobulin-like C2-type domains.

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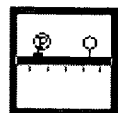
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	U90716; AAC51234.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF169366; AAF05908.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
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	AF169365; AAF05908.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]

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 AF242865; AAG01088.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 AF242862; AAG01088.1; JOINED. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
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 BC003684; AAH03684.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 BC010536; AAH10536.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 1EAJ; 13-JUL-01. [[ExPASy](#) / [RCSB](#)]
 1F5W; 08-NOV-00. [[ExPASy](#) / [RCSB](#)]
 1KAC; 24-NOV-99. [[ExPASy](#) / [RCSB](#)]
 Detailed list of linked structures.
 Genew [HGNC:2559; CXADR](#).
 CleanEx [HGNC:2559; CXADR](#).
 MIM [602621 \[NCBI / EBI\]](#).
 GeneCards [CXADR](#).
 GeneLynx [CXADR; Homo sapiens](#).
 GO [GO:0005887; Cellular component: integral to plasma membrane \(traceable author statement\)](#).
 GO [GO:0004872; Molecular function: receptor activity \(traceable author statement\)](#).
 SOURCE [CXADR; Homo sapiens](#).
 Ensembl [P78310; Homo sapiens. \[Entry / Contig view\]](#)
 InterPro [IPR007110; Ig-like](#).
 InterPro [IPR003598; Ig_c2](#).
 InterPro [Graphical view of domain structure](#).
 Pfam [PF00047; ig; 2](#).
 SMART [SM00408; IGc2; 1](#).
 PROSITE [PS50835; IG_LIKE; 2](#).
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Keywords

Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.

Features



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Key	From	To	Length	Description
SIGNAL	1	19	19	POTENTIAL.

CHAIN	<u>20</u>	<u>365</u>	346	COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
DOMAIN	<u>20</u>	<u>237</u>	218	EXTRACELLULAR (POTENTIAL).
TRANSMEM	<u>238</u>	<u>258</u>	21	POTENTIAL.
DOMAIN	<u>259</u>	<u>365</u>	107	CYTOPLASMIC (POTENTIAL).
DOMAIN	<u>20</u>	<u>134</u>	115	IG-LIKE C2-TYPE 1.
DOMAIN	<u>141</u>	<u>228</u>	88	IG-LIKE C2-TYPE 2.
DISULFID	<u>41</u>	<u>120</u>		BY SIMILARITY.
DISULFID	<u>162</u>	<u>212</u>		BY SIMILARITY.
CARBOHYD	<u>106</u>	<u>106</u>		N-LINKED (GLCNAC...) (POTENTIAL).
CARBOHYD	<u>201</u>	<u>201</u>		N-LINKED (GLCNAC...) (POTENTIAL).

Sequence information

Length: **365 AA** [This is the length of the unprocessed precursor]

Molecular weight: **40029 Da** [This is the MW of the unprocessed precursor]

CRC64: **AB01C6346CB7FE64** [This is a checksum on the sequence]

10	20	30	40	50	60
MALLLCFVLL	CGVVDFAFSL	SITTPEEMIE	KAKGETAYLP	CKFTLSPEDQ	GPLDIEWLIS
70	80	90	100	110	120
PADNQKVDQV	IILYSGDKIY	DDYYPDLKGR	VHFTSNDLKS	GDASINVTNL	QLSDIGTYQC
130	140	150	160	170	180
KVKKAPGVAN	KKIHLVVLVK	PSGARCVDG	SEEIGSDFKI	KCEPKESLP	LQYEWQKLS
190	200	210	220	230	240
SQKMPTSWLA	EMTSSVISVK	NASSEYSGTY	SCTVRNRVGS	DQCLLRNLVV	PPSNKAGLIA
250	260	270	280	290	300
GAIIGTLLAL	ALIGLIIFCC	RKKRREEKYE	KEVHHDIRED	VPPPKSRTST	ARSYIGSNHS
310	320	330	340	350	360
SLGSMSPSNM	EGYSKTQYNQ	VPSEDFERTP	QSPTLPPAKV	AAPNLSRMGA	IPVMIPAQSK

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